



IFWO

RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/678,588A

TIME: 11:50:53

Input Set : D:\52578C_cor.ST25.txt

Output Set: N:\CRF4\10122004\J678588A.raw

3 <110> APPLICANT: Wu, Jingrui
 5 <120> TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants
 7 <130> FILE REFERENCE: 38-21(52578)C
 9 <140> CURRENT APPLICATION NUMBER: US 10/678,588A
 10 <141> CURRENT FILING DATE: 2003-10-02
 12 <150> PRIOR APPLICATION NUMBER: US 60/415,758
 13 <151> PRIOR FILING DATE: 2002-10-02
 15 <150> PRIOR APPLICATION NUMBER: US 60/425,157
 16 <151> PRIOR FILING DATE: 2002-11-08
 18 <150> PRIOR APPLICATION NUMBER: US 60/463,787
 19 <151> PRIOR FILING DATE: 2003-04-11
 21 <160> NUMBER OF SEQ ID NOS: 10
 23 <170> SOFTWARE: PatentIn version 3.2
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2480
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: transcriptional unit comprising promoter, coding sequence for
 32 transcription factor of SEQ ID NO:2 and terminator elements
 34 <400> SEQUENCE: 1

35 aggatattaa agtatgtatt catcattaat ataatcagtg tattccaata tgtactacga 60
 37 tttccaatgt ctttattgtc gccgatgtga atcggcgtca caaaataatc cccggtgact 120
 39 ttcttttaaat ccaggatgaa ataatatgtt attataattt ttgcgatttg gtccgttata 180
 41 ggaattgaag tgtgcttgag ctcggtcgcc accactccca ttccataatt ttacatgtat 240
 43 ttgaaaaata aaaatttatg gtattcaatt taaacacgta tacttgtaaa gaatgatatc 300
 45 ttgaaagaaa tatagtttaa atattttattg ataaaaataac aagtcaggta ttatagtcca 360
 47 agcaaaaaca taaattttatt gatgcaagtt taaattcaga aatatttcaa taactgatta 420
 49 tatcagctgg tacattgccg tagatgaaag actgagtgcg atattatgtg taatacataa 480
 51 attgatgata tagctagaac tagtggtacc cccggggcct gcaggctcga gctagtttga 540
 53 gatatccccg ttatggtact ggggttgcat ataaccatt ccttggttg atgctccctg 600
 55 ttggcccatc ccttggtcag ctgagctact tgctcccaca tgaccaaggg catccttttt 660
 57 aattgagcca tcgctagatt ttgcagttaa cttgctatca cctccatct ctctgtactt 720
 59 ctgcaggtag accctgagg gttcaatgta gtcttcaaac cccagcgtgg ccatggccca 780
 61 cagcagatcg tcgccattga tggcttccg cttctccctc tggcacttg cactcgcttc 840
 63 gctagtgatg aaggagatga actcggagac gcactcctgc acggtctcct tagcgctcct 900
 65 ggcgatcttc ccgttagccg ggatggtctt cccgttagcc gggatggcct tcttcatgat 960
 67 gcgactgatg ttggcgatgg gcaggaacct gtctgtctcc ctgacgctgc caccgcctcc 1020
 69 gctccccctg gggtccccgc tctcgtgggt cccgcgcgcg ccgcccagggc tcgcccggagc 1080
 71 ttccgccatg gtctacctac aaaaaagctc cgacagaggc tgcatttgct acaaatcatg 1140
 73 aaaagaaaaa ctaccgatga acaatgctga gggattcaaa ttctaccac aaaaagaaga 1200
 75 aagaaagatc tagcacatct aagcctgacg aagcagcaga aatatataaa aatataaacc 1260
 77 atagtgcctt tttccctct tctgatctt gtttagcatg gcggaaattt taaaccccc 1320

ENTERED

P. 6

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79 atcatctccc ccaacaacgg cggatcgag atctacatcc gagagcccca ttccccgcga 1380
81 gatccggggc ggatccacgc cggcgagagc cccagccgcg agatcccgcc cctcccgcg 1440
83 accgatctgg gcgcgcacga agccgcctct cgcccaccca aactaccaag gccaaagatc 1500
85 gagaccgaga cggaaaaaaa aaacggagaa agaaagagga gaggggaggg gtggttaccg 1560
87 gcggcgggcg agggggaggg gggaggagct cgtcgtccgg cagcgagggg ggaggaggtg 1620
89 gtggtggtgg tgggtgtagg gttgggggga tgggaggaga ggggggggta tgtatatagt 1680
91 ggcgatgggg ggcgttttct tggaaagcga gggaggggcg gcctcgtcgc tggctcgcga 1740
93 tcctcctcgc gtttccggcc cccacgacct ggaccacct gctgtttttt ctttttcttt 1800
95 tttttctttt tttttttttt tttggctgcg agacgtgagg tgcgtgagg caactcacgg 1860
97 tgatagtggg ggggtgtgga gactattgtc cagttggctg gactggggtg ggttgggttg 1920
99 ggttgggttg ggctgggctt gctatggatc gtggatagca ctttgggctt taggacttta 1980
101 ggggttgttt ttgtaaagt tttgagtcta agtttatctt ttatttttac tagaaaaaat 2040
103 acccatgcgc tgcaacgggg gaaagctatt ttaatcttat tattgttcat tgtgagaatt 2100
105 cgctgaata tatatttttc tcaaaaatta tgtcaaatta gcatatgggt ttttttaaag 2160
107 atattttcta tacaaatccc tctgtattta caaaagcaaa cgaacttaaa acccgactca 2220
109 aatacagata tgcatttcca aaagcgaata aacttaaaaa ccaattcata caaaaatgac 2280
111 gtatcaaagt accgacaaaa acatcctcaa tttttataat agtagaaaag agtaaatttc 2340
113 actttgggcc accttttatt accgatattt tactttatac caccttttaa ctgatgtttt 2400
115 cacttttgac caggaatct tacctttgtt ttattttgga ctatcccgac tctcttctca 2460
117 agcatatgaa tgacctcgag 2480

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120 <210> SEQ ID NO: 2

121 <211> LENGTH: 185

122 <212> TYPE: PRT

123 <213> ORGANISM: Zea mays

125 <400> SEQUENCE: 2

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127 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
128 1 5 10 15
131 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
132 20 25 30
135 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
136 35 40 45
139 Ile Pro Ala Asn Gly Lys Thr Ile Pro Ala Asn Gly Lys Ile Ala Lys
140 50 55 60
143 Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
144 65 70 75 80
147 Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
148 85 90 95
151 Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
152 100 105 110
155 Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
156 115 120 125
159 Glu Gly Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys
160 130 135 140
163 Lys Asp Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Gln Gly
164 145 150 155 160
167 Met Gly Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
168 165 170 175
171 Gln Tyr His Asn Gly Asp Ile Ser Asn
172 180 185

```

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175 <210> SEQ ID NO: 3
176 <211> LENGTH: 178
177 <212> TYPE: PRT
178 <213> ORGANISM: Zea mays
180 <400> SEQUENCE: 3
182 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
183 1 5 10 15
186 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
187 20 25 30
190 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
191 35 40 45
194 Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
195 50 55 60
198 Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
199 65 70 75 80
202 Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
203 85 90 95
206 Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
207 100 105 110
210 Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr
211 115 120 125
214 Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val
215 130 135 140
218 Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly Gln Gln Gly Ala Tyr
219 145 150 155 160
222 Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile
223 165 170 175
226 Ser Asn

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230 <210> SEQ ID NO: 4
231 <211> LENGTH: 537
232 <212> TYPE: DNA
233 <213> ORGANISM: Zea mays
235 <400> SEQUENCE: 4
236 atggcggaag ctccggcgag ccctggcggc ggcggcgggg gccacgagag cgggagcccc 60
238 aggggaggcg gaggcggtgg cagcgtcagg gagcaggaca gggtcctgcc catcgccaac 120
240 atcagtcgca tcatgaagaa ggccatcccg gctaacggga agatcgccaa ggacgctaag 180
242 gagaccgtgc aggagtgcgt ctccgagttc atctccttca tcactagcga agcgagtgc 240
244 aagtgccaga gggagaagcg gaagaccatc aatggcgacg atctgctgtg ggccatggcc 300
246 acgctggggg ttgaagacta cattgaaccc ctcaagggtg acctacagaa gtacagagag 360
248 atggagggtg atagcaagtt aactgctaaa tctagcgatg gctcgattaa aaaggatgct 420
250 cttggtcatg tgggagcaag tagctcagct gcagaaggga tgggccaaca gggagcatac 480
252 aaccaaggaa tgggttatat gcaacctcag taccataacg gggatatctc aaactaa 537

```

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255 <210> SEQ ID NO: 5
256 <211> LENGTH: 522
257 <212> TYPE: DNA
258 <213> ORGANISM: Glycine max
260 <400> SEQUENCE: 5
261 atgtcggatg cgccaccgag cccgactcat gagagtgggg gcgagcagag cccgcgcggt 60
263 tcgtcgtccg gcgcgaggga gcaggaccgg tacctcccga ttgccaacat cagccgcatt 120

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```

265 atgaagaagg ctctgcctcc caacggcaag attgcaaagg atgccaaaga caccatgcag 180
267 gaatgcgttt ctgagttcat cagcttcatt accagcgagg cgagtgagaa atgccagaag 240
269 gagaagagaa agacaatcaa tggagacgat ttgctatggg ccatggccac tttaggattt 300
271 gaagactaca tagagccgct taagggtgtac ctggctaggt acagagaggc ggagggtgac 360
273 actaaaggat ctgctagaag tggatgatga tctgctacac cagatcaagt tggccttgca 420
275 ggtcaaaatt ctcagcttgt tcatcagggt tcgctgaact atattggttt gcaggtgcaa 480
277 ccacaacatc tggttatgcc ttcaatgcaa agccatgaat ag 522

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280 <210> SEQ ID NO: 6

281 <211> LENGTH: 173

282 <212> TYPE: PRT

283 <213> ORGANISM: Glycine max

285 <400> SEQUENCE: 6

287 Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln

288 1 5 10 15

291 Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu

292 20 25 30

295 Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn

296 35 40 45

299 Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser

300 50 55 60

303 Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys

304 65 70 75 80

307 Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala

308 85 90 95

311 Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala

312 100 105 110

315 Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly

316 115 120 125

319 Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser

320 130 135 140

323 Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln

324 145 150 155 160

327 Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu

328 165 170

331 <210> SEQ ID NO: 7

332 <211> LENGTH: 141

333 <212> TYPE: PRT

334 <213> ORGANISM: Arabidopsis thaliana

336 <400> SEQUENCE: 7

338 Met Ala Asp Thr Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly

339 1 5 10 15

342 Gly Ser Val Arg Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser

343 20 25 30

346 Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp

347 35 40 45

350 Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile

351 50 55 60

354 Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val

355 65 70 75 80

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```

358 Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
359           85           90           95
362 Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
363           100           105           110
366 Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
367           115           120           125
370 Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
371           130           135           140

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374 <210> SEQ ID NO: 8

375 <211> LENGTH: 101

376 <212> TYPE: PRT

377 <213> ORGANISM: Artificial sequence

379 <220> FEATURE:

380 <223> OTHER INFORMATION: protein consensus sequence

383 <220> FEATURE:

384 <221> NAME/KEY: MISC_FEATURE

385 <222> LOCATION: (22)..(22)

386 <223> OTHER INFORMATION: Xaa can be Ala or Pro

388 <220> FEATURE:

389 <221> NAME/KEY: MISC_FEATURE

390 <222> LOCATION: (26)..(26)

391 <223> OTHER INFORMATION: Xaa can be Thr or none

393 <220> FEATURE:

394 <221> NAME/KEY: MISC_FEATURE

395 <222> LOCATION: (27)..(27)

396 <223> OTHER INFORMATION: Xaa can be Ile or none

398 <220> FEATURE:

399 <221> NAME/KEY: MISC_FEATURE

400 <222> LOCATION: (28)..(28)

401 <223> OTHER INFORMATION: Xaa can be Pro or none

403 <220> FEATURE:

404 <221> NAME/KEY: MISC_FEATURE

405 <222> LOCATION: (29)..(29)

406 <223> OTHER INFORMATION: Xaa can be Ala or none

408 <220> FEATURE:

409 <221> NAME/KEY: MISC_FEATURE

410 <222> LOCATION: (30)..(30)

411 <223> OTHER INFORMATION: Xaa can be Asn or none

413 <220> FEATURE:

414 <221> NAME/KEY: MISC_FEATURE

415 <222> LOCATION: (31)..(31)

416 <223> OTHER INFORMATION: Xaa can be Gly or none

418 <220> FEATURE:

419 <221> NAME/KEY: MISC_FEATURE

420 <222> LOCATION: (32)..(32)

421 <223> OTHER INFORMATION: Xaa can be Lys or none

423 <220> FEATURE:

424 <221> NAME/KEY: MISC_FEATURE

425 <222> LOCATION: (39)..(39)

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 22,26,27,28,29,30,31,32,39,41,58,62,94,95,99

Seq#:9; Xaa Pos. 29

Seq#:10; Xaa Pos. 2,3,4,6

VERIFICATION SUMMARY

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Input Set : D:\52578C_cor.ST25.txt

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L:464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:32
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:80
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0